# EAST Search History

| Ref # | Hits | Search Query | DBs | Default Operator | Plurals | Time Stamp |
|---|---|---|---|---|---|---|
| L1 | 30 | evolut$ near10 bottlen$ | US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB | OR | ON | 2007/03/13 19:32 |
| L2 | 1247752 | @rlad<"20030808" | US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB | OR | ON | 2007/03/13 19:32 |
| L3 | 10 | l1 and l2 | US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB | OR | ON | 2007/03/13 19:32 |

3/13/07

Serial No. 10/522,393

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James Martinell
Primary Examiner 1634

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 NEWS 6 MAR 03 MEDLINE and LMEDLINE reloaded
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available on STN
 NEWS 10 MAR 29 WPIFV now available on STN
 NEWS 11 MAR 29 No connect hour charges in WPIFV until May
1, 2004
 NEWS 12 MAR 29 New monthly current-awareness alert (SDI)
frequency in RAPRA
 NEWS 13 APR 26 PROMT: New display field available
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display field          available
 NEWS 15 APR 26 LITALERT now available on STN
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TOTAL                                 ENTRY   SESSION
FULL ESTIMATED COST                    0.06      0.27

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TOTAL                                 ENTRY   SESSION
FULL ESTIMATED COST                    0.21      0.48

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FILE LAST UPDATED: 26 Apr 2004  (20040426/ED)

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=> s (evolut? (3a) bottle?)/bi,ab    311904 EVOLUT?/BI
238375 EVOLUT?/AB                    36832 BOTTLE?/BI
32803 BOTTLE?/AB
L1          60 (EVOLUT? (3A) BOTTLE?)/BI,AB

=> s l1 not 2004/py    343365 2004/PY
L2          58 L1 NOT 2004/PY

=> d his
 (FILE 'HOME' ENTERED AT 14:11:25 ON 27 APR 2004)
 FILE 'STNGUIDE' ENTERED AT 14:11:30 ON 27 APR 2004
 FILE 'HOME' ENTERED AT 14:11:35 ON 27 APR 2004
 FILE 'CAPLUS' ENTERED AT 14:11:44 ON 27 APR 2004
L1          60 S (EVOLUT? (3A) BOTTLE?)/BI,AB
L2          58 S L1 NOT 2004/PY
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3/13/07

=> s (evolut? (3a) bottlen?)/bi,ab 311904 EVOLUT?/BI
238375 EVOLUT?/AB 3651 BOTTLEN?/BI
3424 BOTTLEN?/AB
L3 42 (EVOLUT? (3A) BOTTLEN?)/BI,AB

=> d his
(FILE 'HOME' ENTERED AT 14:11:25 ON 27 APR 2004)
FILE 'STNGUIDE' ENTERED AT 14:11:30 ON 27 APR 2004
FILE 'HOME' ENTERED AT 14:11:35 ON 27 APR 2004
FILE 'CAPLUS' ENTERED AT 14:11:44 ON 27 APR 2004
L1 60 S (EVOLUT? (3A) BOTTLE?)/BI,AB
L2 58 S L1 NOT 2004/PY
L3 42 S (EVOLUT? (3A) BOTTLEN?)/BI,AB

=> d l3 1-42 bib ab

L3 ANSWER 1 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2004:316950 CAPLUS
TI Genetic diversity in cowpea [Vigna unguiculata (L.) Walp.] as revealed by RAPD markers
AU Ba, Fana Sylla; Pasquet, Remy S.; Gepts, Paul
CS B.P., Dakar-Hann, 15226, Senegal
SO Genetic Resources and Crop Evolution (2004), 51(5), 539-550 CODEN: GRCEE9; ISSN: 0925-9864
PB Kluwer Academic Publishers
DT Journal
LA English
AB The present study, using RAPD anal., was undertaken to characterize genetic variation in domesticated cowpea and its wild progenitor, as well as their relationships. The materials used consisted of 26 domesticated accessions, including accessions from each of the five cultivar-group, and 30 wild/weedy accessions, including accessions from West, East and southern Africa. A total of 28 primers generated 202 RAPD bands. One hundred and eight bands were polymorphic among the domesticated compared to 181 among wild/weedy cowpea accessions. Wild accessions were more diverse in East Africa, which is the likely area of origin of V. unguiculata var. spontanea. Var. spontanea is supposed to have spread westward and southward, with a loss of variability, loss counterbalanceed in southern Africa by introgressions with local perennial subspecies. Although the variabilty of domesticated cowpea was the highest ever recorded, cultivar-groups were poorly resolved, and several results obtained with isoenzyme data were not confirmed here. However primitive cultivars were more diverse than evolved cultivars, which still suggests two consecutive ***bottlenecks*** within domesticated cowpea ***evolution*** . As isoenzymes and AFLP markers, although with a larger no. of markers, RAPD data confirmed the single domestication hypothesis, the gap between wild and domesticated cowpea, and the widespread introgression phenomena between wild and domesticated cowpea.

L3 ANSWER 2 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2004:311054 CAPLUS
TI Detection of ***evolutionary*** ***bottlenecking*** by DNA sequencing as a method to discover genes of value
IN Messier, Walter
PA Evolutionary Genomics, LLC, USA
SO PCT Int. Appl., 46 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2004031397 A2 20040415 WO 2003-US25027 20030808 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2002-402340P P 20020808
AB This invention relates to using molecular and evolutionary techniques to identify polynucleotide and polypeptide sequences corresponding to commercially or aesthetically relevant traits in domesticated plants and animals, specifically, a method to detect ***evolutionary*** ***bottleneck*** sequences.

L3 ANSWER 3 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:976675 CAPLUS
DN 140:142838
TI The effects of population bottlenecks on genetic diversity and rates of molecular evolution in Spheniscus penguins
AU Akst, Elaine Pincus
CS Univ. of Maryland, College Park, MD, USA
SO (2002) 78 pp. Avail.: UMI, Order No. DA3078382 From: Diss. Abstr. Int., B 2003, 64(1), 49
DT Dissertation
LA English
AB Unavailable

L3 ANSWER 4 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:715212 CAPLUS
DN 140:232733
TI Effects of intense versus diffuse population bottlenecks on microsatellite genetic diversity and evolutionary potential
AU England, Phillip R.; Osler, Graham H. R.; Woodworth, Lynn M.; Montgomery, Margaret E.; Briscoe, David A.; Frankham, Richard
CS Department of Biological Sciences, Key Centre for Biodiversity and Bioresources, Macquarie University, NSW 2109, Australia
SO Conservation Genetics (2003), 4(5), 595-604 CODEN: CGOEAC; ISSN: 1566-0621
PB Kluwer Academic Publishers
DT Journal
LA English
AB Population bottlenecks occur frequently in threatened species and result in loss of genetic diversity and evolutionary potential. These may range in severity between short intense bottlenecks, and more diffuse bottlenecks over many generations. However, there is little information on the impacts of different types of bottlenecks and disagreement as to their likely impacts. To resolve this issue, we subjected replicate Drosophila populations to intense bottlenecks, consisting of 1 pair over a single generation, vs. diffuse bottlenecks consisting of an effective size of 100 over 57 generations. The intense and diffuse bottlenecks were designed to induce identical losses of heterozygosity. However, computer simulations showed that the probability of retaining alleles is lower in the intense than the diffuse bottleneck treatment. The effects of these bottlenecks on genetic diversity at 9 microsatellite loci in Drosophila were evaluated. Bottlenecks substantially reduced allelic diversity, heterozygosity, and proportion of loci polymorphic, changed allele frequency distributions and resulted in large differences among replicate populations. Allelic diversity, scaled by heterozygosity,

was lower in the intense than the diffuse treatments. Short-term evolutionary potential, measured as the ability of bottlenecked populations to cope with increasing concns. of NaCl, did not differ between the intense and diffuse bottlenecked populations. The effects of ***bottlenecks*** on short-term ***evolutionary*** potential relate to loss of heterozygosity, rather than allelic diversity.
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 5 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:581731 CAPLUS
DN 139:256930
TI Three-dimensional functional model proteins: Structure function and evolution
AU Blackburne, Benjamin P.; Hirst, Jonathan D.
CS School of Chemistry, University of Nottingham, Nottingham, NG7 2RD, UK
SO Journal of Chemical Physics (2003), 119(6), 3453-3460 CODEN: JCPSA6; ISSN: 0021-9606
PB American Institute of Physics
DT Journal
LA English
AB The mapping of phenotype onto genotype for a set of functional model proteins is accomplished by exhaustive enumeration on a three-dimensional diamond lattice. Chains of up to 25 monomers are investigated and their evolution characterized. The model is used to investigate the origins of designability. Highly designable functional model protein structures possess contact maps that have a relatively little commonality with other phys. allowed contact maps. Although the diamond lattice has the same coordination no. as the square lattice, differences between three-dimensional and two-dimensional functional model proteins are obsd. One difference is the lower frequency of structures of low designability on the three-dimensional lattice. In other respects, the conclusions drawn from previous studies using the square lattice remain valid in three dimensions. For example, we observe the tendency for longer chains to form larger networks of sequences with greater stability to mutation. We identify various topog. characteristics of the landscapes: ***evolutionary*** ***bottlenecks*** bridge otherwise unconnected networks, and hub sequences allow rapid movement between the different neutral networks. The diversity of landscapes that arises from even a minimalist model suggests that real proteins have a rich variety of evolutionary landscapes.
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 6 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:420389 CAPLUS
DN 139:161995
TI Modeling bacterial evolution with comparative-genome-based marker systems: Application to Mycobacterium tuberculosis evolution and pathogenesis
AU Alland, David; Whittam, Thomas S.; Murray, Megan B.; Cave, M. Donald; Hazbon, Manzour H.; Dix, Kim; Kokoris, Mark; Duesterhoeft, Andreas; Eisen, Jonathan A.; Fraser, Claire M.; Fleischmann, Robert D.
CS Department of Medicine, Center for Emerging Pathogens, New Jersey Medical School, Newark, NJ, 07103, USA
SO Journal of Bacteriology (2003), 185(11), 3392-3399 CODEN: JOBAAY; ISSN: 0021-9193
PB American Society for Microbiology
DT Journal
LA English
AB The comparative-genomic sequencing of two Mycobacterium tuberculosis strains enabled us to identify single nucleotide polymorphism (SNP) markers for studies of evolution, pathogenesis, and epidemiol. in clin. M. tuberculosis. Phylogenetic anal. using these "comparative-genome markers" (CGMs) produced a highly unusual phylogeny with a complete absence of secondary branches. To investigate CGM-based phylogenies, we devised computer models to simulate sequence evolution and calc. new phylogenies based on an SNP format. We found that CGMs represent a distinct class of phylogenetic markers that depend critically on the genetic distances between compared "ref. strains.". Properly distanced ref. strains generate CGMs that accurately depict evolutionary relationships, distorted only by branch collapse. Improperly distanced ref. strains generate CGMs that distort and reroot outgroups. Applying this understanding to the CGM-based phylogeny of M. tuberculosis, we found evidence to suggest that this species is highly clonal without detectable lateral gene exchange. We noted indications of ***evolutionary*** ***bottlenecks*** , including one at the level of the PHRI "C" strain previously assocd. with particular virulence characteristics. Our evidence also suggests that loss of IS6110 to fewer than seven elements per genome is uncommon. Finally, we present population-based evidence that KasA, an important component of mycolic acid biosynthesis, develops G312S polymorphisms under selective pressure.
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 7 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:864005 CAPLUS
DN 138:184317
TI Allozyme and microsatellite diversity in natural and domestic populations of turbot (Scophthalmus maximus) in comparison with other Pleuronectiformes
AU Bouza, C.; Presa, P.; Castro, J.; Sanchez, L.; Martinez, P.
CS Departamento de Genetica, Facultad de Veterinaria, Universidad de Santiago de Compostela, Lugo, 27002, Spain
SO Canadian Journal of Fisheries and Aquatic Sciences (2002), 59(9), 1460-1473 CODEN: CJFSDX; ISSN: 0706-652X
PB National Research Council of Canada
DT Journal
LA English
AB Twelve microsatellite and 28 allozyme loci were employed to analyze genetic diversity in natural and domestic populations of turbot (S. maximus) from northwest Spain in comparison with other flatfish species with similar habitat, life history, and geog. distribution: the brill (S. rhombus) and the flounder (Platichthys flesus). These species had shown much higher allozyme diversity than turbot in previous studies, and were used as a ref. to check for putative historical bottlenecks in turbot. Significantly lower genetic variability in turbot than in brill and flounder was confirmed with allozymes, but not with the highly variable microsatellite loci. This intermarker discrepancy could be explained by different mutation rates in relation with historical ***bottlenecks*** along turbot ***evolution*** . A significantly lower genetic diversity was obsd. in a domestic strain of turbot than in natural populations of this species. This sample evidenced a strong family structure from microsatellite data, which suggests caution against the use of com. batches for broodstock foundation in turbot farming. A strong concordance was found across the 2 categories of markers used when analyzing the pattern of genetic subdivision at a local scale within

the 3 species analyzed, low and nonsignificant genetic differentiation being obsd. between Atlantic and Cantabric areas.
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 8 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:842835 CAPLUS
DN 138:119765
TI Compensatory adaptation to the deleterious effect of antibiotic resistance in Salmonella typhimurium
AU Maisnier-Patin, Sophie; Berg, Otto G.; Liijas, Lars; Andersson, Dan I.
CS Department of Bacteriology, Swedish Institute for Infectious Disease Control, Solna, S-171 82, Swed.
SO Molecular Microbiology (2002), 46(2), 355-366 CODEN: MOMIEE; ISSN: 0950-382X
PB Blackwell Science Ltd.
DT Journal
LA English
AB Most chromosomal mutations that cause antibiotic resistance impose fitness costs on the bacteria. This biol. cost can often be reduced by compensatory mutations. In Salmonella typhimurium, the nucleotide substitution AAA42 .fwdarw. AAC in the rpsL gene confers resistance to streptomycin. The resulting amino acid substitution (K42N) in ribosomal protein S12 causes an increased rate of ribosomal proofreading and, as a result, the rate of protein synthesis, bacterial growth and virulence are decreased. Eighty-one independent lineages of the low-fitness, K42N mutant were evolved in the absence of antibiotic to ameliorate the costs. From the rate of fixation of compensated mutants and their fitness, the rate of compensatory mutations was estd. to be .gtoreq.10-7 per cell per generation. The size of the population ***bottleneck*** during ***evolution*** affected fitness of the adapted mutants: a larger bottleneck resulted in higher av. fitness. Only four of the evolved lineages contained streptomycin-sensitive revertants. The remaining 77 lineages contained mutants that were still fully streptomycin resistant, had retained the original resistance mutation and also acquired compensatory mutations. Most of the compensatory mutations, resulting in at least 35 different amino acid substitutions, were novel single-nucleotide substitutions in the rpsD, rpsE, rpsL or rplS genes encoding the ribosomal proteins S4, S5, S12 and L19, resp. Our results show that the deleterious effects of a resistance mutation can be compensated by an unexpected variety of mutations.
RE.CNT 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 9 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:840914 CAPLUS
DN 138:301029
TI Genetic Diversity and Fitness in Black-Footed Ferrets Before and During a Bottleneck
AU Wisely, S. M.; Buskirk, S. W.; Fleming, M. A.; McDonald, D. B.; Ostrander, E. A.
CS Department of Zoology and Physiology, University of Wyoming, Laramie, WY, 82071, USA
SO Journal of Heredity (2002), 93(4), 231-237 CODEN: JOHEA8; ISSN: 0022-1503
PB Oxford University Press
DT Journal
LA English
AB The black-footed ferret (Mustela nigripes) is an endangered North American carnivore that underwent a well-documented population bottleneck in the mid-1980s. To better understand the effects of a bottleneck on a free-ranging carnivore population, we used 24 microsatellite loci to compare genetic diversity before vs. during the bottleneck, and compare the last wild population to two historical populations. We also compared genetic diversity in black-footed ferrets to that of two sibling species, the steppe polecat (Mustela eversmanni) and the European polecat (Mustela putorius). Black-footed ferrets during the bottleneck had less genetic diversity than steppe polecats. The three black-footed ferret populations were well differentiated (FST = 0.57 .+-. 0.15; mean .+-. SE). We attributed the decrease in genetic diversity in black-footed ferrets to localized extinction of these genetically distinct subpopulations and to the bottleneck in the surviving subpopulation. Although genetic diversity decreased, female fecundity and juvenile survival were not affected by the population bottleneck.
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 10 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:623880 CAPLUS
TI Modeling viral genome fitness ***evolution*** associated with serial ***bottleneck*** events: Evidence of stationary states of fitness
AU Lazaro, Ester; Escarmis, Cristina; Domingo, Esteban; Manrubia, Susanna C.
CS Centro de Astrobiologia (CSIC-INTA), Madrid, 28850, Spain
SO Journal of Virology (2002), 76(17), 8675-8681 CODEN: JOVIAM; ISSN: 0022-538X
PB American Society for Microbiology
DT Journal
LA English
AB Evolution of fitness values upon replication of viral populations is strongly influenced by the size of the virus population that participates in the infections. While large population passages often result in fitness gains, repeated plaque-to-plaque transfers result in av. fitness losses. Here we develop a numerical model that describes fitness evolution of viral clones subjected to serial bottleneck events. The model predicts a biphasic evolution of fitness values in that a period of exponential decrease is followed by a stationary state in which fitness values display large fluctuations around an av. const. value. This biphasic evolution is in agreement with exptl. results of serial plaque-to-plaque transfers carried out with foot-and-mouth disease virus (FMDV) in cell culture. The existence of a stationary phase of fitness values has been further documented by serial plaque-to-plaque transfers of FMDV clones that had reached very low relative fitness values. The statistical properties of the stationary state depend on several parameters of the model, such as the probability of advantageous vs. deleterious mutations, initial fitness, and the no. of replication rounds. In particular, the size of the bottleneck is crit. for detg. the trend of fitness evolution.
RE.CNT 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 11 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:418733 CAPLUS
DN 138:183030
TI A novel type of uracil-DNA glycosylase mediating repair of hydrolytic DNA damage in the extremely thermophilic eubacterium Thermus thermophilus
AU Starkuviene, Vytaute; Fritz, Hans-Joachim

CS Abteilung Molekulare Genetik und Praparative Molekularbiologie and Gottingen Genomics Laboratory, Institut fur Mikrobiologie und Genetik, Georg-August-Universitat, Gottingen, D-37077, Germany
SO Nucleic Acids Research (2002), 30(10), 2097-2102 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB Spontaneous hydrolytic deamination of DNA cytosine and 5-methyl-cytosine residues is an abundant source of C/G (5-meC/G) to T/A transition mutations. As a result of this pressure, at least six different families of enzymes have evolved that initiate repair at U/G (T/G) mispairs, the relevant pre-mutagenic intermediates. The necessarily higher rate of the process at elevated temps. must pose a correspondingly accentuated problem to contemporary thermophilic organisms and may have been a serious ***bottleneck*** in early ***evolution*** when life passed through a phase of very high ambient temps. Here we show that Thermus thermophilus, an aerobic, Gram-neg. eubacterium thriving at up to 85.degree., harbors two uracil-DNA glycosylases (UDGs), termed TTUDGA and TTUDGB. According to both amino acid sequence and enzymic properties, TTUDGA clearly belongs to the family of "thermostable UDGs". TTUDGB shares with TTUDGA 23% sequence identity, but differs from it in profound functional aspects. TTUDGB, unlike TTUDGA, does not act upon uracil residues in the context of single-stranded DNA whereas both enzymes process various double-stranded substrates, albeit with different preferences. TTUDGB shows a no. of sequence features characteristic of the UDG super-family, but surprisingly lacks any polar residue within its so-called motif 1 (GLAPG-X10-F). This finding is in conflict with a previously assumed crucial catalytic role of motif 1 in water activation and supports a more recently suggested alternative of a dissociative ("SN1-type") reaction mechanism. Together, the characteristics of TTUDGB and its homologs in other organisms define a novel family of UDG repair enzymes.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 12 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:390191 CAPLUS
DN 137:229529
TI Paraphyly in Hawaiian hybrid blowfly populations and the evolutionary history of anthropophilic species
AU Stevens, J. R.; Wall, R.; Wells, J. D.
CS School of Biological Sciences, University of Exeter, Exeter, EX4 4PS, UK
SO Insect Molecular Biology (2002), 11(2), 141-148 CODEN: IMBIE3; ISSN: 0962-1075
PB Blackwell Science Ltd.
DT Journal
LA English
AB Complementary nuclear (28S rRNA) and mitochondrial (COI + II) gene markers were sequenced from the blowflies, Lucilia cuprina and Lucilia sericata, from Europe, Africa, North America, Australasia and Hawaii. Populations of the two species were phylogenetically distinct at both genes, with one exception. Hawaiian L. cuprina possessed typical L. cuprina-type rRNA, but had L. sericata-type mitochondrial (COI + II) sequences. An explanation for this pattern is that Hawaiian flies are hybrids and comparison of obsd. levels of sequence divergence to possible introduction events, e.g. Polynesian colonization, suggests that Hawaiian L. cuprina may be evolving rapidly. Moreover, the monophyly of these flies also suggests that the L. sericata mtDNA haplotype was apparently fixed in Hawaiian L. cuprina by lineage sorting, indicating a population ***bottleneck*** in the ***evolutionary*** history of these island flies.
RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 13 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:321877 CAPLUS
DN 137:91088
TI Genetic diversity of a Capsicum germplasm collection from Nepal as determined by randomly amplified polymorphic DNA markers
AU Baral, J.; Bosland, P. W.
CS Department of Agronomy and Horticulture, MSC 3Q, New Mexico State University, Las Cruces, NM, 88003-0003, USA
SO Journal of the American Society for Horticultural Science (2002), 127(3), 318-324 CODEN: JOSHB5; ISSN: 0003-1062
PB American Society for Horticultural Science
DT Journal
LA English
AB Domesticated chile (Capsicum annuum L. var. annuum) is a widely cultivated spice and vegetable crop. It originated in the Western Hemisphere, but spread rapidly throughout the globe after the voyage of Columbus. However, very little is known about the genetic diversity of chile in Asia and esp. in Nepal. Thus, research was conducted to document morphol. as well as mol. characterization of C. annuum var. annuum landraces collected from Nepal. Genetic diversity in C. annuum var. annuum landraces from Nepal was investigated using randomly amplified polymorphic DNA (RAPD) markers and compared with that of C. annuum var. annuum landraces from the center of diversity, Mexico. RAPD marker based cluster anal. of C. annuum var. annuum clearly sepd. each accession. All accessions of C. annuum var. annuum from Nepal grouped into a single cluster at a similarity index value of 0.80, whereas, accessions from Mexico grouped into eight different clusters at the same similarity level indicating greater genetic diversity in Mexican accessions. RAPD anal. indicated that the Nepalese chile population went through an addnl. ***evolutionary*** ***bottleneck*** or founder effect probably due to intercontinental migrations. Some Nepalese accessions had unique RAPD markers suggesting that addnl. sources of genetic variation are available in Nepalese germplasm.
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 14 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:825530 CAPLUS
DN 137:17614
TI A genetic ***bottleneck*** in the " ***evolution*** under domestication" of upland cotton Gossypium hirsutum L. examined using DNA fingerprinting
AU Iqbal, M. J.; Reddy, O. U. K.; El-Zik, K. M.; Pepper, A. E.
CS Department of Soil and Crop Sciences, Texas A and M University, College Station, TX, 77843-2474, USA
SO Theoretical and Applied Genetics (2001), 103(4), 547-554 CODEN: THAGA6; ISSN: 0040-5752
PB Springer-Verlag
DT Journal
LA English
AB Reliable information about the evolutionary and genetic relationships of various germplasm resources is essential to the establishment of rational strategies for crop improvement. We used AFLPs to study the genetic relationships of 43 cultivars of

Gossypium hirsutum representative of the genomic compn. of modern "Upland" cotton. The study also included representatives of the related tetraploid species Gossypium barbadense, as well as the diploid species Gossypium raimondii, Gossypium incanum, Gossypium herbaceum and Gossypium arboreum. We tested 20 primer combinations that resulted in a total of 3,178 fragments. At the species level, and above, genetic similarities based on AFLPs were in agreement with the known taxonomic relationships. Similarity indexes ranged from 0.25 to 0.99. Representatives of the G. hirsutum germplasm resources utilized in North America, including secondary accessions collected by breeders in Central America ("Acala", "Tuxtla", "Kekchi") and the southwestern US ("Hopi Moencopi"), formed a single cluster with exceedingly limited genetic diversity (with many pairwise similarity indexes >0.96) We concluded that these accessions were derived from the same genetic pool. The early maturing or "latifolium" or "Mexican Highlands" cultigens from which these cultivars were derived appear to have had extremely limited genetic diversity, perhaps as a result of a severe genetic bottleneck resulting from the selection pressures of domestication. Outside of the major G. hirsutum cluster, well-supported phylogenies were inferred. Inside this cluster, phylogenies were obscured by limited diversity, reticulation and lineage sorting. The implications of these findings for cotton improvement are discussed.
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 15 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:130995 CAPLUS
DN 135:301496
TI The Geographic Distribution of Monoamine Oxidase Haplotypes Supports a Bottleneck During the Dispersion of Modern Humans from Africa
AU Balciuniene, Jorune; Syvanen, Anne-Christine; McLeod, Howard L.; Pettersson, Ulf; Jazin, Elena E.
CS Section of Medical Genetics, Department of Genetics and Pathology, Rudbeck Laboratory, Uppsala University, Uppsala, SE-751 85, Swed.
SO Journal of Molecular Evolution (2001), 52(2), 157-163 CODEN: JMEVAU; ISSN: 0022-2844
PB Springer-Verlag New York Inc.
DT Journal
LA English
AB Every genetic locus mingles the information about the evolutionary history of the human species with the history of its own evolution. Therefore, to address the question of the origin of humans from a genetic point of view, evolutionary histories from many genetic loci have to be gathered and compared. The authors studied two genes residing on the X chromosome encoding monoamine oxidases A and B (MAOA and MAOB). Both genes have been suggested to play a role in psychiatric and/or behavioral traits. To search for DNA variants of the MAO genes, the sequences of exonic and flanking intronic regions of these two genes were detd. in a group of Swedish males. The sequence anal. revealed several novel polymorphisms in the MAO genes. Haplotypes contg. high-frequency MAOA polymorphisms were constructed, and their frequencies were detd. in addnl. samples from Caucasian, Asian, and African populations. We found two common haplotypes with similar frequencies in Caucasian and Asian populations. However, only one of them was also the most frequent haplotype in Africans, while the other haplotype was present in only one Kenyan male. This profound change in haplotype frequencies from Africans to non-Africans supports a possible bottleneck during the dispersion of modern humans from Africa.
RE.CNT 63 THERE ARE 63 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 16 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:82784 CAPLUS
DN 135:267919
TI Isolation and characterization of microsatellite DNA markers in the Florida manatee (Trichechus manatus latirostris) and their application in selected sirenian species
AU Garcia-Rodriguez, A. I.; Moraga-Amador, D.; Farmerie, W.; Mcguire, P.; King, T. L.
CS Biological Resources Division, Sirenia Project, United States Geological Survey, Gainesville, FL, 32601, USA
SO Molecular Ecology (2000), 9(12), 2161-2163 CODEN: MOECEO; ISSN: 0962-1083
PB Blackwell Science Ltd.
DT Journal
LA English
AB Fourteen sets of primers amplified fragments of expected size from Florida manatee genomic DNA. These markers were screened in 50 manatees collected throughout the Florida peninsula. Eight of the 14 loci were polymorphic in this initial survey, and overall levels of heterozygosity averaged 41%. Low levels of allelic diversity were obsd. in the Florida manatee. The max. no. of alleles identified was six (TmaEll), and the av. no. of alleles obsd. at polymorphic loci was 2.9. This paucity of genetic diversity suggests a founder effect or major population ***bottleneck*** of ***evolutionary*** significance. In addn., this study reports one of the lowest levels of genetic diversity obsd. in species-specific microsatellite DNA markers. Cross-species amplification was tested in three Sirenian taxa: the Antillean manatee (T. m. manatus), the Amazonian manatee (T. inunguis) and the dugong (Dugong dugong). Eleven of 14 markers were polymorphic for the Antillean and the Amazonian manatee. At least nine markers were polymorphic in the dugong; the polymorphism is likely to be under-estd. due to the small sample size (n = 3). This suite of markers appears to be ideal for the identification of population structure and possibly pedigree anal. in all four Sirenian species, and provides a nuclear DNA-based approach to complement existing mitochondrial DNA genetic information for these vulnerable.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 17 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:80760 CAPLUS
DN 135:148066
TI Global patterns of human DNA sequence variation in a 10-kb region on chromosome 1
AU Yu, Ning; Zhao, Z.; Fu, Y.-X.; Sambuughin, N.; Ramsay, M.; Jenkins, T.; Leskinen, E.; Patthy, L.; Jorde, L. B.; Kuromori, T.; Li, W.-H.
CS Department of Ecology and Evolution, University of Chicago, Chicago, IL, 60637, USA
SO Molecular Biology and Evolution (2001), 18(2), 214-222 CODEN: MBEVEO; ISSN: 0737-4038
PB Society for Molecular Biology and Evolution
DT Journal
LA English
AB Human DNA variation is currently a subject of intense research because of its importance for studying human origins, evolution, and demog. history and for assocn. studies of complex

diseases. A .apprx.10-kb region on chromosome 1, which contains only four small exons (each < 155 bp), was sequenced for 61 humans (20 Africans, 20 Asians, and 21 Europeans) and for 1 chimpanzee, 1 gorilla, and 1 orangutan. We found 52 polymorphic sites among the 122 human sequences and 382 variant sites among the human, chimpanzee, gorilla, and orangutan sequences. For the introns sequenced (8,991 bp), the nucleotide diversity (.pi.) was 0.058% among all sequences, 0.076% among the African sequences, 0.047% among the Asian sequences, and 0.045% among the European sequences. A compilation of data revealed that autosomal regions have, on av., the highest .pi. value (0.091%), X-linked regions have a somewhat lower .pi. value (0.079%), and Y-linked regions have a very low .pi. value (0.008%). The lower polymorphism in the present region may be due to a lower mutation rate and/or selection in the gene contg. these introns or in genes linked to this region. The present region and two other 10-kb noncoding regions all show a strong excess of low-frequency variants, indicating a relatively recent population expansion. This region has a low mutation rate, which was estd. to be 0.74 .times. 10-9 per nucleotide per yr. An av. est. of .apprx.12,600 for the long-term effective population size was obtained using various methods; the est. was not far from the commonly used value of 10,000. Fu and Li's tests rejected the assumption of an equil. neutral Wright-Fisher population, largely owing to the high proportion of low-frequency variants. The age of the most recent common ancestor of the sequences in our sample was estd. to be more than 1 Myr. Allowing for some unrealistic assumptions in the model, this est. would still suggest an age of more than 500,000 yr, providing further evidence for a genetic history of humans much more ancient than the emergence of modern humans. The fact that many unique variants exist in Europe and Asia also suggests a fairly long genetic history outside of Africa and argues against a complete replacement of all indigenous populations in Europe and Asia by a small Africa stock. Moreover, the ancient genetic history of humans indicates no severe ***bottleneck*** during the ***evolution*** of humans in the last half million years; otherwise, much of the ancient genetic history would have been lost during a severe bottleneck. We suggest that both the "Out of Africa" and the multiregional models are too simple to explain the evolution of modern humans.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 18 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:798908 CAPLUS
DN 134:53627
TI Population structure of rat-derived Pneumocystis carinii in Danish wild rats
AU Palmer, Robert J.; Settnes, Osvald P.; Lodal, Jens; Wakefield, Ann E.
CS Molecular Infectious Diseases Group, Department of Paediatrics, Institute of Molecular Medicine, John Radcliffe Hospital, Oxford, OX3 9DS, UK
SO Applied and Environmental Microbiology (2000), 66(11), 4954-4961 CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
AB The rat model of Pneumocystis carinii pneumonia is frequently used to study human P. carinii infection, but there are many differences between the rat and human infections. We studied naturally acquired P. carinii in wild rats to examine the relevance of the rat model for human infection. P. carinii DNA was detected in 47 of 51 wild rats and in 10 of 12 nonimmunosuppressed lab. rats. Evidence for three novel formae speciales of rat-derived P. carinii was found, and these were provisionally named Pneumocystis carinii f. sp. rattus-secundi, Pneumocystis carinii f. sp. rattus-tertii, and Pneumocystis carinii f. sp. rattus-quarti. Our data suggest that low-level carriage of P. carinii in wild rats and nonimmunosuppressed lab. rats is common and that wild rats are frequently coinfected with more than one forma specialis of P. carinii. We also examd. the diversity in the internally transcribed spacer (ITS) regions of the nuclear rRNA operon of Pneumocystis carinii f. sp. carinii by using samples from wild rats and lab. rats and spore trap samples. We report a lack of variation in the ITS1 and ITS2 regions that is consistent with an ***evolutionary*** ***bottleneck*** in the P. carinii f. sp. carinii population. This study shows that human- and rat-derived P. carinii organisms are very different, not only in genetic compn. but also in population structure and natural history.
RE.CNT 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 19 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:789360 CAPLUS
DN 135:103316
TI Experimental evaluation of the usefulness of microsatellite DNA for detecting demographic bottlenecks
AU Spencer, C. C.; Neigel, J. E.; Leberg, P. L.
CS Department of Biology, University of Louisiana at Lafayette, Lafayette, LA, 70504, USA
SO Molecular Ecology (2000), 9(10), 1517-1528 CODEN: MOECEO; ISSN: 0962-1083
PB Blackwell Science Ltd.
DT Journal
LA English
AB Evolutionary and conservation biologists often use mol. markers to evaluate whether populations have experienced demog. bottlenecks that resulted in a loss of genetic variation. We evaluated the utility of microsatellites for detection of recent, severe bottlenecks and compared the amts. of genetic diversity lost in bottlenecks of different sizes. In exptl. mesocosms, we established replicate populations by releasing 1, 2, 4 or 8 pairs of the western mosquitofish, Gambusia affinis (Poeciliidae). Using eight polymorphic microsatellite loci, we quantified seven indexes of genetic diversity or change that have been used to assess the effects of demog. bottlenecks on populations. We compared indexes for the exptl. bottlenecked populations to those for the source population and examd. differences between populations established with different nos. of founders. Direct count heterozygosity and the proportion of polymorphic loci were not very sensitive to genetic changes that resulted from the exptl. bottlenecks. Heterozygosity excess and expected heterozygosity were useful to varying degrees in the detection of bottlenecks. Allelic diversity and temporal variance in allele frequencies were most sensitive to genetic changes that resulted from the bottlenecks, and the temporal variance method was slightly more correlated with bottleneck size than was allelic diversity. Based on comparisons to a previous study with allozymes, heterozygosity, temporal variance in allele frequencies and allelic diversity, but not proportion of polymorphic loci, appear to be more sensitive to demog. bottlenecks when quantified using microsatellites. We found that anal. of eight highly polymorphic loci was sufficient to detect a recent demog. bottleneck and to obtain an est. of the magnitude of bottleneck severity.

RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 20 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:759892 CAPLUS
DN 134:336554
TI Worldwide DNA sequence variation in a 10-kilobase noncoding region on human chromosome 22
AU Zhao, Zhongming; Jin, Li; Fu, Yun-Xin; Ramsay, Michele; Jenkins, Trefer; Leskinen, Elina; Pamilo, Pekka; Trexler, Maria; Patthy, Laszlo; Jorde, Lynn B.; Ramos-Onsins, Sebastian; Yu, Ning; Li, Wen-Hsiung
CS Human Genetics Center, University of Texas Health Science Center-Houston, Houston, TX, 77030, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2000), 97(21), 11354-11358 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Human DNA sequence variation data are useful for studying the origin, evolution, and demog. history of modern humans and the mechanisms of maintenance of genetic variability in human populations, and for detecting linkage assocn. of disease. Here, we report worldwide variation data from a .apprxeq.10-kilobase noncoding autosomal region. We identified 75 variant sites in 64 humans (128 sequences) and 463 variant sites among the human, chimpanzee, and orangutan sequences. Statistical tests suggested that the region is selectively neutral. The av. nucleotide diversity (.pi.) across the region was 0.088% among all of the human sequences obtained, 0.085% among African sequences, and 0.082% among non-African sequences, supporting the view of a low nucleotide diversity (.apprxeq.0.1%) in humans. The comparable .pi. value in non-Africans to that in Africans indicates no severe ***bottleneck*** during the ***evolution*** of modern non-Africans; however, the possibility of a mild bottleneck cannot be excluded because non-Africans showed considerably fewer variants than Africans. The present and two previous large data sets all show a strong excess of low frequency variants in comparison to that expected from an equil. population, indicating a relatively recent population expansion. The mutation rate was estd. to be 1.15 .times. 10-9 per nucleotide per yr. Ests. of the long-term effective population size Ne by various statistical methods were similar to those in other studies. The age of the most recent common ancestor was estd. to be .apprxeq.1.29 million years ago among all of the sequences obtained and .apprxeq.634,000 yr ago among the non-African sequences, providing the first evidence from a noncoding autosomal region for ancient human histories, even among non-Africans.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 21 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:714583 CAPLUS
DN 134:3077
TI Absence of a genetic bottleneck in a wild rabbit (Oryctolagus cuniculus) population exposed to a severe viral epizootic
AU Queney, G.; Ferrand, N.; Marchandeau, S.; Azevedo, M.; Mougel, F.; Branco, M.; Monnerot, M.
CS Centre de Genetique Moleculaire (CGM), CNRS, Gif sur Yvette, 91198, Fr.
SO Molecular Ecology (2000), 9(9), 1253-1264 CODEN: MOECEO; ISSN: 0962-1083
PB Blackwell Science Ltd.
DT Journal
LA English
AB Infectious diseases and their demog. consequences are thought to influence the genetic diversity of populations. In Europe, during the last 50 yr, the European rabbit (Oryctolagus cuniculus) has suffered two important viral epizootics: myxomatosis and rabbit viral hemorraghic disease (RVHD). Although mortality rates were very high, the impact of these diseases on genetic diversity has never been assessed directly. The subject of this paper is a wild rabbit population in France, which has been studied since the beginning of the 1980s. The first outbreak of RVHD occurred in 1995 and provoked a demog. crash. The population, sampled for the first time in 1982 and 1994, was sampled again at the end of 1996 to examine the impact of the epizootic on genetic diversity. In spite of the obsd. high mortality rate (.apprxeq. 90%), anal. of 14 polymorphic loci (allozymes and microsatellites) showed no loss in genetic diversity after the epizootic. Detn. of temporal changes in allele frequencies indicated that the population evolved under genetic drift. The temporal method of Waples demonstrated a significant decrease in the effective population size (Ne) correlated with the demog. crash due to the epizootic. However, the population had only been studied for two generations after the epizootic and the remnant population size probably stayed high enough (.apprxeq. 50 individuals) to keep its genetic diversity at the precrash level. These results suggest that, contrary to what is usually thought and in spite of the subsequent high mortality rates, past epizootics (esp. myxomatosis) may have had little effect on the genetic diversity of wild rabbit populations in Europe.
RE.CNT 81 THERE ARE 81 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 22 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:509811 CAPLUS
DN 134:112687
TI Hepatitis C virus RNA codes for proteins and replicates: Does it also trigger the interferon response?
AU Branch, Andrea D.
CS Division of Liver Diseases, Department of Medicine, Recanati/Miller Transplantation Institute, Mount Sinai School of Medicine, New York, NY, 10029, USA
SO Seminars in Liver Disease (2000), 20(1), 57-68 CODEN: SLDIEE; ISSN: 0272-8087
PB Thieme Medical Publishers, Inc.
DT Journal; General Review
LA English
AB A review with 99 refs. Hepatitis C virus (HCV) is a pos. sense virus with a genomic RNA mol. roughly 9600 nucleotides in length. The single-stranded genomic RNA has a nontranslated region (NTR) at each end and a long open reading frame (coding region) in between. The 5'NTR and portions of the 3'NTR are the most conserved parts of HCV RNA. These conserved regions contain signals for replication and translation. Much of the 5'NTR is folded into a structure that binds ribosomes. This structure, an internal ribosome entry site, promotes the initiation of protein synthesis and is crit. for HCV gene expression. During replication, the genomic RNA is copied by virally encoded enzymes into a complementary antigenomic RNA, which itself is a template for the synthesis of progeny RNAs. HCV RNA replication is thought to take place in the cytoplasm and is an error-prone process. Natural selection acts upon the progeny RNAs, causing the population to change and drift. Over time, mutation, selection, and population ***bottlenecks*** led to the ***evolution*** of varied genotypes. The HCV replication

complex is a potential source of double-stranded RNA, a powerful inducer of interferon. Thus, HCV-specific double-stranded RNA may trigger the first steps of innate immunity; however, for unknown reasons, the immune system often fails to clear the infection. The plasticity of the HCV genome and the low level of HCV gene expression may counterbalance any immunostimulatory effects of HCV RNA and allow the virus to escape specific immune responses. Antisense drugs and ribozymes directed against HCV RNA are under investigation.
RE.CNT 99 THERE ARE 99 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 23 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:478989 CAPLUS
DN 134:203373
TI Detecting bottlenecks and selective sweeps from DNA sequence polymorphism
AU Galtier, Nicolas; Depaulis, Frantz; Barton, Nicholas H.
CS Institute of Cell, Animal and Population Biology, University of Edinburgh, Edinburgh, EH9 3JT, UK
SO Genetics (2000), 155(2), 981-987 CODEN: GENTAE; ISSN: 0016-6731
PB Genetics Society of America
DT Journal
LA English
AB A coalescence-based max.-likelihood method is presented that aims to (i) detect diversity-reducing events in the recent history of a population and (ii) distinguish between demog. (e.g., bottlenecks) and selective causes (selective sweep) of a recent redn. of genetic variability. The former goal is achieved by taking account of the distortion in the shape of gene genealogies generated by diversity-reducing events: gene trees tend to be more star-like than under the std. coalescent. The latter issue is addressed by comparing patterns between loci: demog. events apply to the whole genome whereas selective events affect distinct regions of the genome to a varying extent. The max.-likelihood approach allows one to est. the time and strength of diversity-reducing events and to choose among competing hypotheses. An application to sequence data from an African population of Drosophila melanogaster shows that the bottleneck hypothesis is unlikely and that one or several selective sweeps probably occurred in the recent history of this population.
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 24 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:81994 CAPLUS
DN 132:180056
TI Population ***bottlenecks*** and Pleistocene human ***evolution***
AU Hawks, John; Hunley, Keith; Lee, Sang-Hee; Wolpoff, Milford
CS Department of Anthropology, University of Utah, USA
SO Molecular Biology and Evolution (2000), 17(1), 2-22 CODEN: MBEVEO; ISSN: 0737-4038
PB Society for Molecular Biology and Evolution
DT Journal; General Review
LA English
AB The anatomical and archaeol. evidence for an early population bottleneck in humans and bracket the time when it could have occurred. The subsequent demog. changes that the archaeol. evidence of range expansions and contractions address are outlined. It is also examd. how inbreeding effective population size provides an alternative view of past population size change. This addresses the question of other, more recent, population size bottlenecks, and the nonrecombining and recombining genetic systems that may reflect them are reviewed. It is studied how these genetic data constrain the possibility of significant population size bottlenecks at several different crit. times in human history. Different constraints appear in nonrecombining and recombining systems, and among the autosomal loci most are incompatible with any Pleistocene population size expansions. Microsatellite data seem to show Pleistocene population size expansions, but in aggregate they are difficult to interpret because different microsatellite studies do not show the same expansion. The archaeol. data are only compatible with a few of these analyses, most prominently with data from Alu elements, and these facts are used to question whether the view of the past from anal. of inbreeding effective population size is valid. Finally, the issue of whether inbreeding effective population size provides any reasonable measure of the actual past size of the human species is examd.
RE.CNT 205 THERE ARE 205 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 25 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:457623 CAPLUS
DN 131:240913
TI A human population bottleneck can account for the discordance between patterns of mitochondrial versus nuclear DNA variation
AU Fay, Justin C.; Wu, Chung-I.
CS Committee on Genetics, University of Chicago, Chicago, IL, 60637, USA
SO Molecular Biology and Evolution (1999), 16(7), 1003-1005 CODEN: MBEVEO; ISSN: 0737-4038
PB Society for Molecular Biology and Evolution
DT Journal
LA English
AB The authors found using computer simulations that the apparently incongruent patterns of mitochondrial and nuclear variation are quite compatible with a recent human population bottleneck. Passing through the same bottleneck, the mitochondrial genome experiences a greater redn. in levels of variation, but recovers more quickly than the nuclear genome. The opposite skews in the frequency distribution of mitochondrial and nuclear variation found in extant human populations are not necessarily incompatible with a common history shared by the two genomes.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 26 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:296023 CAPLUS
DN 129:3279
TI The Finnish population ***bottleneck*** : exploiting the ***evolutionary*** history of genes for population and genetic disease studies
AU Kittles, Ricky Antonius
CS George Washington Univ., Washington, DC, USA
SO (1998) 126 pp. Avail.: UMI, Order No. DA9817622 From: Diss. Abstr. Int., B 1998, 58(12), 6369
DT Dissertation
LA English
AB Unavailable

L3 ANSWER 27 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:662597 CAPLUS

DN 127:327264
TI Phylogenetic relationships among bottlenose dolphins (genus Tursiops) in a worldwide context (Stenella, Delphinus, mitochondrial DNA)
AU Curry, Barbara Edith
CS Texas A and M Univ., College Station, TX, USA
SO (1997) 138 pp. Avail.: UMI, Order No. DA9729178 From: Diss. Abstr. Int., B 1997, 58(4), 1657
DT Dissertation
LA English
AB Unavailable

L3 ANSWER 28 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:536704 CAPLUS
DN 127:200864
TI Historical demography and present day population structure of the greenfinch, Carduelis chloris-an analysis of mtDNA control-region sequences
AU Merila, Juha; Bjorklund, Mats; Baker, Allan J.
CS Department of Zoology, Uppsala University, Uppsala, S-752 36, Swed.
SO Evolution (Lawrence, Kansas) (1997), 51(3), 946-956
CODEN: EVOLAO; ISSN: 0014-3820
PB Society for the Study of Evolution
DT Journal
LA English
AB Genetic variability within and among 10 geog. distinct populations of Greenfinches (Carduelis chloris) was assayed by directly sequencing a 637 BP part of the mtDNA control region from 194 individuals. Thirteen variable positions defined 18 haplotypes with a max. sequence divergence of 0.8%. Haplotype (h = 0.28-0.77) and nucleotide (.pi. = 0.058-0.17%) diversities within populations were low, and decreased with increasing latitude (h:rs = -0.81; .pi.: rs = -0.89). The distribution of pairwise nucleotide differences fit better with expectations of a "sudden expansion" than of an "equil." model, and the ests. of long term effective population sizes were considerably lower than current census ests., esp. in northern European samples. Selection is an unlikely cause of obsd. patterns because the distribution of variability conformed to expectations of neutral infinite alleles model and haplotype diversity across populations was pos. correlated with heterozygosity (HE) in nuclear genes (rs = 0.74, P < 0.05). Hence, a recent bottleneck, followed by serial bottlenecking during the process of post-Pleistocene recolonization of northern Europe, together with recent population expansion provide a plausible explanation for the low genetic diversity in the north. Genetic distances among populations showed a clear pattern of isolation-by- distance, and 14% of the haplotypic variation was among populations, the rest being distributed among individuals within populations. In accordance with allozyme and morphol. data, a hierarchical anal. of nucleotide diversity recognized southern European populations as distinct from northern European ones. However, the magnitude of divergence in mtDNA, allozymes and morphol. were highly dissimilar (morphol. > mtDNA > allozymes).

L3 ANSWER 29 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:319782 CAPLUS
DN 126:339527
TI Intraspecific variation in mitochondrial DNA of muskoxen, based on control-region sequences
AU Groves, Pamela
CS Institute of Arctic Biology, University of Alaska Fairbanks, Fairbanks, AK, 99775-7000, USA
SO Canadian Journal of Zoology (1997), 75(4), 568-575
CODEN: CJZOAG; ISSN: 0008-4301
PB National Research Council of Canada
DT Journal
LA English
AB The muskox (Ovibos moschatus) is thought to have experienced significant genetic bottlenecks. Despite these bottlenecks, two subspecies of muskox, O. m. wardi and O. m. moschatus, have been commonly accepted, based on morphol. differences and geog. sepn. The reintroduction of muskoxen to Alaska from Greenland has created a situation in which the proposed subspecies might meet and interbreed as the Alaskan (O. m. wardi) and mainland Canadian (O. m. moschatus) populations expand their ranges. To attempt to define subspecific differences and investigate the appropriateness of potential interbreeding of Alaskan and Canadian mainland muskoxen, control-region sequences of mitochondrial DNA were compared among 37 muskoxen. Extremely little variation was found among all the muskoxen sampled. These results do not allow definition of muskox subspecies and suggest that the different populations may already have mixed. The low levels of variability further support historical and archaeol. evidence of repeated bottlenecks throughout the history of the species.

L3 ANSWER 30 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:269525 CAPLUS
DN 126:313725
TI The length distribution of perfect dimer repetitive DNA is consistent with its evolution by an unbiased single-step mutation process
AU Bell, George I.; Jurka, Jerzy
CS Theoretical Biology and Biophysics Group, MS K710, Los Alamos National Laboratory, Los Alamos, NM, 87545, USA
SO Journal of Molecular Evolution (1997), 44(4), 414-421
CODEN: JMEVAU; ISSN: 0022-2844
PB Springer
DT Journal
LA English
AB We have examd. the length distribution of perfect dimer repeats, where perfect means uninterrupted by any other base, using data from GenBank on primates and rodents. Virtually no lengths greater than 30 repeats are found, except for rodent AG repeats, which extend to 35. Comparable nos. of long AC and AG repeats suggest that they have not been selected for special functions or DNA structures. We have compared the data with predictions of two models: (1) a Bernoulli Model in which bases are assumed equally likely and distributed at random and (2) an Unbiased Random Walk Model (URWM) in which repeats are permitted to change length by plus or minus one unit, with equal probabilities, and in which base substitutions are allowed to destroy long perfect repeats, producing two shorter perfect repeats. The source of repeats is assumed to be from single base substitutions from neighboring sequences, i.e., those differing from the perfect repeat by a single base. Mutation rates either independent of repeat length or proportional to length were considered. An upper limit to the lengths L .apprxeq. 30 is assumed and isolated dimers are assumed unable to expand, so that there are absorbing barriers to the random walk at lengths 1 and L + 1, and a steady state of lengths is reached. With these assumptions and estd. values for the rates of length mutation and base substitution, reasonable agreement is found with the data for lengths > 5 repeats. Shorter repeats, of lengths .ltoreq. 3 are in general agreement with the Bernoulli Model. By reducing the rate of length mutations for n .ltoreq. 5, it is possible to obtain reasonable agreement with the full range of data. For these reduced rates, the times between length mutations become comparable to those suggested for a

***bottleneck*** in the ***evolution*** of Homo sapiens, which may be the reason for low heterozygosity of short repeats.

L3 ANSWER 31 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:145919 CAPLUS
DN 126:184275
TI Simulation models of bottleneck events in natural populations
AU Halley, John; Hoelzel, A. Rus
CS NERC Cent. Population Biol., Imperial Coll., Ascot/Berks., UK
SO Molecular Genetic Approaches in Conservation (1996), 347-364. Editor(s): Smith, Thomas B.; Wayne, Robert K. Publisher: Oxford University Press, New York, N. Y. CODEN: 63ZNAN
DT Conference; General Review
LA English
AB The authors discuss how simulation models can be used to study the development of natural populations. They show how consequent genetic effects can be used to infer the characteristics of a bottleneck and compare models based on mitochondrial DNA with those based on nuclear DNA. Three examples are dicussed: the Northern elephant seal following the bottleneck of 1884; the Ngorongoro crater lions following the Stomoxys epidemic in 1962; and the Asian lions in the Gir forest.

L3 ANSWER 32 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:46466 CAPLUS
DN 126:101831
TI Allozyme diversity in the endangered shrub Lindera melissifolia (Lauraceae) and its widespread congener Lindera benzoin
AU Godt, Mary Jo W.; Hamrick, J. L.
CS Departments of Botany and Genetics, University of Georgia, Athens, GA, 30602, USA
SO Canadian Journal of Forest Research (1996), 26(12), 2080-2087 CODEN: CJFRAR; ISSN: 0045-5067
PB National Research Council of Canada
DT Journal
LA English
AB Allozyme diversity was assessed in 15 populations of the endangered clonal shrub Lindera melissifolia (Walt.) Blume (pondberry; Lauraceae) throughout its range in the southeastern United States and in five populations of spicebush (Lindera benzion (L.) Blume), a sexually reproducing, co-occurring congener. Low levels of allozyme variation characterize both dioecious species. Although genetic diversity was moderately high (HT = 0.239) at polymorphic loci for L. benzoin, few of the 42 loci were polymorphic (Ps = 35%; Pp = 25%),and thus overall ests. of genetic diversity were relatively low (hes = 0.083; Hep = 0.070). Little genetic variation was detected at 27 loci within L. melissifolia loci (33%) were polymorphic but genetic diversity was low (hT = 0.074) at these loci, and few were polymorphic within populations (mean 6.7%). The no. of multilocus genotypes detected in L. melissifolia populations ranged from t to 18, with a mean of 4.5. Mean genetic identities between populations within each species were high (I = 0.98 and 0.99 for L. benzlin and L. melissifolia, resp.), a result of the high nos. of monomorphic loci. Despite the high genetic similarity of populations, ests. of gene flow were low to moderate (Nm = 0.82 and 1.25 for L. melissifolia and L. benzoin, resp.). The lower diversity within L. melissifolia may be primarily due to ***bottlenecks*** during its ***evolutionary*** history. The recent loss of populations and of genets within populations have probably further eroded genetic diversity. To reduce the risk of extinction, effective population sizes of L. melissifolia could be enhanced by increasing genotypic diversity within populations.

L3 ANSWER 33 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:735238 CAPLUS
DN 126:15414
TI Repeated transfer of small RNA virus populations leading to balanced fitness with infrequent stochastic drift
AU Novella, Isabel S.; Elena, Santiago F.; Moya, Andres; Domingo, Esteban; Holland, John J.
CS Department biology and Institute Molecular Genetics, University California, San diego, La Jolla, CA, 92093-0116, USA
SO Molecular & General Genetics (1996), 252(6), 733-738 CODEN: MGGEAE; ISSN: 0026-8925
PB Springer
DT Journal
LA English
AB The population dynamics of RNA viruses have an important influence on fitness variation and, in consequence, on the adaptative potential and virulence of this ubiquitous group of pathogens. Earlier work with vesicular stomatitis virus showed that large population transfers were reproducibly assocd. with fitness increases, whereas repeated transfers from plaque to plaque (genetic bottlenecks) lead to losses in fitness. We demonstrate here that repeated five-plaque to five-plaque passage series yield long-term fitness stability, except for occasional stochastic fitness jumps. Repeated five-plaque passages regularly alternating with two consecutive large population transmissions did not cause fitness losses, but did limit the size of fitness gains that would otherwise have occurred. These results underscore the profound effects of ***bottleneck*** transmissions in virus ***evolution*** .

L3 ANSWER 34 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:227296 CAPLUS
DN 124:280734
TI Intratype variation in 12 human papillomavirus types: a worldwide perspective
AU Stewart, Ann-Charlotte M.; Eriksson, Annika M.; Manos, M. Michele; Munoz, Nubia; Bosch, F. Xavier; Peto, Julian; Wheeler, Cosette M.
CS Dep. Cell Biol., Univ. New Mexico Sch. Med., Albuquerque, NM, 87131, USA
SO Journal of Virology (1996), 70(5), 3127-36 CODEN: JOVIAM; ISSN: 0022-538X
PB American Society for Microbiology
DT Journal
LA English
AB In this study, we have examd. intratype human papillomavirus (HPV) sequence variation in a worldwide collection of cervical specimens. Twelve different HPV types including HPV-18, HPV-33, HPV-35, HPV-39, HPV-45, HPV-51, HPV-52, HPV-58, HPV-59, HPV-68 (ME180), MM9/PAP238A (recently designated HPV-73), and a novel partial genomic HPV sequence designated MM4/W13B were analyzed in this study. Cervical specimens were collected as part of epidemiol. investigations conducted in New Mexico and an internal study of invasive cervical cancer (IBSCC). Specimens from several countries including Argentina, Brazil, Bolivia, Benin, Cuba, Colombia, Chile, Germany, Mali, Panama, Paraguay, Spain, Algeria, Uganda, Guinea, Tanzania, Indonesia, Philippines, Thailand, and the United States were evaluated. Specimen DNAs were subjected to amplification with the MY09/11 L1 consensus PCR system. The PCR products were cloned, and an approx. 410-bp region in the L1 open reading frame was sequenced from 146 specimens (.apprx.60,000 bp). Within a single HPV type, nucleotide diversity varied between 0.2 and 2.9% (i.e., between any pair of variants) and the majority of nucleotide changes were synonymous (amino acid conserving). These data provide information pertinent to HPV diagnostic probe development and are potentially relevant to future rational

vaccine strategies. Similarly, amino acid diversity varied between 0 and 5.1%. Some of these amino acid changes may represent markers of intertype evolutionary relationships. Presuming that HPVs have evolved under the same constraints as their corresponding hosts, the limited genetic diversity obsd. for all HPVs studied to date may reflect an ***evolutionary*** ***bottleneck*** occurring in both virus and host populations.

L3 ANSWER 35 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:208835 CAPLUS
DN 124:251912
TI The evolution of human populations: A molecular perspective
AU Ayala, Francisco J.; Escalante, Ananias A.
CS Department Ecology and Evolutionary Biology, University California, Irvine, CA, 92717, USA
SO Molecular Phylogenetics and Evolution (1996), 5(1), 188-201 CODEN: MPEVEK; ISSN: 1055-7903
PB Academic
DT Journal; General Review
LA English
AB A review with 80 refs. Human evolution exhibits repeated speciations and conspicuous morphol. change: from Australopithecus to Homo habilis, H. erectus, and H. sapiens; and from their hominoid ancestor to orangutans, gorillas, chimpanzees, and humans. Theories of founder event speciation propose that speciation often occurs as a consequence of population bottlenecks, down to one or very few individual pairs. Proponents of punctuated equil. claim in addn. that founder event speciation results in rapid morphol. change. The major histocompatibility complex (MHC) consists of several very polymorphic gene loci. The genealogy of 19 human alleles of the DQB1 locus coalesces more than 30 million years ago, before the divergence of apes and Old World monkeys. Many human alleles are more closely related to pongid and cercopithecoid alleles than to other human alleles. Using the theory of gene coalescence, we est. that these polymorphisms require human populations of the order of N = 100,000 individuals for the last several million years. This conclusion is confirmed by computer simulations showing the rate of decay of the polymorphisms over time. Computer simulations indicate, in addn., that in human ***evolution*** no ***bottlenecks*** have occurred with fewer than several thousand individuals. We evaluate studies of mtDNA, Y-chromosome, and microsatellite autosomal polymorphisms and conclude that they are consistent with the MHC result that no narrow population bottlenecks have occurred in human evolution. The available mol. information favors a recent African origin of modern humans, who spread out of Africa approx. 100,000 to 200,000 yr ago.

L3 ANSWER 36 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:560441 CAPLUS
DN 123:2718
TI Mitochondrial DNA diversity in the Kuna Amerinds of Panama
AU Batista, Oriana; Kolman, Connie J.; Bermingham, Eldredge
CS Univ. Costa Rica, Balboa, Panama
SO Human Molecular Genetics (1995), 4(5), 921-9 CODEN: HMGEE5; ISSN: 0964-6906
PB Oxford University Press
DT Journal
LA English
AB Mitochondrial DNA (mtDNA) haplotype diversity was detd. for 63 Chibcha-speaking Kuna Amerinda sampled widely across their geog. range in eastern Panama. The Kuna data were compared with mtDNA control region I sequences from two neighboring Chibchan groups, the Ngobe and the Huetar; two Amerind groups located at the northern and southern extremes of Amerind distribution, the Nuu-Chah-Nulth of the Pacific Northwest and the Chilean Mapuche; and with a single Na-Dene group, the Haida of the Pacific Northwest. The Kuna exhibited low levels of mitochondrial diversity as had been reported for the other two Chihchan groups and, furthermore, carried only two of the four Amerind founding lineages first reported by Schurr and coworkers (Am. J. Hum. Genet. 1990; 46: 613-623). The authors suggest that speakers of modern Chibchan languages (henceforth referred to as the Chibcha) passed through a population bottleneck caused either by ethnogenesis from a small founding population and/or subsequent European conquest and colonization. Using the approach of Harpending et al. (Curr. Anthropol. 1993; 34: 483-496), the authors estd. a Chibchan population bottleneck and subsequent expansion approx. 10 000 yr before present, a date consistent with a bottleneck at the time of Chibchan ethnogenesis. The low mtDnA diversity of Kuna Amerinds, as opposed to the generally high levels of mtDNA variation detected in other Amerind groups, demonstrates the need for adequate sampling of cultural or racial groups when attempting to genetically characterize human populations.

L3 ANSWER 37 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:550836 CAPLUS
DN 123:134784
TI Evolution of tRNA recognition systems and tRNA gene sequences
AU Saks, Margaret E.; Sampson, Jeffrey R.
CS Division of Biology, California Institute of Technology, Pasadena, CA, 91125, USA
SO Journal of Molecular Evolution (1995), 40(5), 509-18 CODEN: JMEVAU; ISSN: 0022-2844
PB Springer
DT Journal
LA English
AB The aminoacylation of tRNAs by the aminoacyl-tRNA synthetases recapitulates the genetic code by dictating the assocn. between amino acids and tRNA anticodons. The sequences of tRNAs were analyzed to investigate the nature of primordial recognition systems and to make inferences about the evolution of tRNA gene sequences and the evolution of the genetic code. Evidence is presented that primordial synthetases recognized acceptor stem nucleotides prior to the establishment of the three major phylogenetic lineages. However, acceptor stem sequences probably did not achieve a level of sequence diversity sufficient to faithfully specify the anticodon assignments of all 20 amino acids. This putative ***bottleneck*** in the ***evolution*** of the genetic code may have been alleviated by the advent of anticodon recognition. A phylogenetic anal. of tRNA gene sequences from the deep Archaea revealed groups that are united by sequence motifs which are located within a region of the tRNA that is involved in detg. its tertiary structure. An assocn. between the third anticodon nucleotide (N36) and these sequence motifs suggests that a tRNA-like structure existed close to the time that amino acid-anticodon assignments were being established. The sequence anal. also revealed that tRNA genes may evolve by anticodon mutations that recruit tRNAs from one isoaccepting group to another. Thus tRNA gene evolution may not always be monophyletic with respect to each isoaccepting group.

L3 ANSWER 38 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:452825 CAPLUS
DN 123:26711
TI Tandem repeat sequence variation and length heteroplasmy in the mitochondrial DNA D-loop of the threatened Gulf of Mexico sturgeon, Acipenser oxyrhynchus desotoi

AU Miracle, A. L.; Campton, D. E.
CS Department of Fisheries and Aquatic Sciences, University of Florida, Gainesville, FL, 32653-3372, USA
SO Journal of Heredity (1995), 86(1), 22-7 CODEN: JOHEA8; ISSN: 0022-1503
DT Journal
LA English
AB Genetic variability within the Suwannee River, Florida, population of Gulf of Mexico sturgeon, Acipenser oxyrhynchus desotoi, was assessed by examg. sequence and length variation within the control region, or D-loop, of the mitochondrial genome. Although once abundant throughout the Gulf of Mexico, Gulf sturgeon are now listed as a threatened species by the U.S. Fish and Wildlife Service. Mitochondrial DNA was analyzed for length variation from 168 individual Gulf sturgeon by PCR amplification and visualization of PCR products using ethidium bromide-stained agarose gels. Of the 168 individual Gulf sturgeon, 31 (18.5%) were heteroplasmic for one to four copies of an 81-base pair, tandemly repeated sequence in the D-loop region. However, no individuals homoplasmic for multiple copies of the repeat sequence were obsd. The existence and nature of these tandem repeats in heteroplasmic individuals was confirmed by direct sequencing of the PCR products for a subset of 22 individuals. The results are consistent with the apparent nature and mechanism of heteroplasmy obsd. in a congeneric species, A. transmontanus. In addn., sequences for 187 base pairs outside of the tandem repeats were identical among all 16 individuals assayed for this region. Lack of variable sequences is concordant with earlier studies involving mtDNA restriction fragment length profiles of Gulf sturgeon found in the Suwannee River. The absence of sequence variation exclusive of the tandem repeats is consistent with the hypothesis that the subspecies has undergone a population or ***evolutionary*** ***bottleneck*** .

L3 ANSWER 39 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1994:4357 CAPLUS
DN 120:4357
TI The genetic drift of human papillomavirus type 16 is a means of reconstructing prehistoric viral spread and the movement of ancient human populations
AU Ho, Lisa; Chan, Shih Yen; Burk, Robert D.; Das, B. C.; Fujinaga, Kei; Icenogle, Joseph P.; Kahn, Tomas; Kiviat, Nancy; Lancaster, Wayne; et al.
CS Inst. Mol. Cell Biol., Natl. Univ. Singapore, Singapore, 0511, Singapore
SO Journal of Virology (1993), 67(11), 6413-23 CODEN: JOVIAM; ISSN: 0022-538X
DT Journal
LA English
AB The authors investigated the diversity of a hypervariable segment of the human papillomavirus type 16 (HPV-16) genome among 301 virus isolates that were collected from 25 different ethnic groups and geog. locations. Altogether, they distinguished 48 different variants that had diversified from one another along five phylogenetic branches. Variants from two of these branches were nearly completely confined to Africa. Variants from a third branch were the only variants identified in Europeans but occurred at lower frequency in all other ethnic groups. A fourth branch was specific for Japanese and Chinese isolates. A small fraction of all isolates from Asia and from indigenous as well as immigrant populations in the Americas formed a fifth branch. Important patterns of HPV-16 phylogeny suggested coevolution of the virus with people of the three major human races, namely, Africans, Caucasians, and East Asians. But several minor patterns are indicative of smaller ***bottlenecks*** of viral ***evolution*** and spread, which may correlate with the migration of ethnic groups in prehistoric times. The colonization of the Americas by Europeans and Africans is reflected in the compn. of their HPV-16 variants. The authors discuss arguments that today's HPV-16 genomes represent a degree of diversity that evolved over a large time span, probably exceeding 200,000 yr, from a precursor genome that may have originated in Africa. The identification of mol. variants is a powerful epidemiol. and phylogenetic tool for revealing the ancient spread of papillomaviruses, whose trace through the world has not yet been completely lost.

L3 ANSWER 40 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1991:676530 CAPLUS
DN 115:276530
TI Low nucleotide diversity in man
AU Li, Wen Hsiung; Sadler, Lori A.
CS Health Sci. Cent., Univ. Texas, Houston, TX, 77225, USA
SO Genetics (1991), 129(2), 513-23 CODEN: GENTAE; ISSN: 0016-6731
DT Journal
LA English
AB The nucleotide diversity (.pi.) in humans is studied by using published cDNA and genomic sequences that have been carefully checked for sequencing accuracy. This measure of genetic variability is defined as the no. of nucleotide differences per site between two randomly chosen sequences from a population. A total of more than 75,000 base pairs from 49 loci are compared. The DNA regions studied are the 5' and 3' untranslated (UT) regions and the amino acid-coding regions. The coding regions are divided into nondegenerate sites (i.e., sites at which all possible changes are nonsynonymous), twofold degenerate sites (i.e., sites at each of which one of the three possible changes is synonymous), and fourfold degenerate sites (i.e., sites at which all three possible changes are synonymous). The .pi. values estd. are, resp., 0.03 and 0.04% for the 5' and 3' UT regions, and 0.03, 0.06 and 0.11% for nondegenerate, twofold degenerate, and fourfold degenerate sites. Since the highest .pi. value is only 0.11%, which is about one order of magnitude lower than those in Drosophila populations, the nucleotide diversity in humans is very low. The low diversity is probably due to a relatively small long-term effective population size rather than any severe ***bottleneck*** during human ***evolution*** .

L3 ANSWER 41 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1991:489751 CAPLUS
DN 115:89751
TI No severe ***bottleneck*** during human ***evolution*** : evidence from two apolipoprotein C-II deficiency alleles
AU Xiong, Weijun; Li, Wen Hsiung; Posner, Israel; Yamamura, Taku; Yamamoto, Akira; Gotto, Antonio M., Jr.; Chan, Lawrence
CS Dep. Med., Baylor Coll. Med., Houston, TX, USA
SO American Journal of Human Genetics (1991), 48(2), 383-9 CODEN: AJHGAG; ISSN: 0002-9297
DT Journal
LA English
AB The DNA sequences of a Japanese and a Venezuelan apolipoprotein (apo) C-II deficiency allele, of a normal Japanese apo C-II gene, and of a chimpanzee apo C-II gene were amplified by the polymerase chain reaction (PCR), and their nucleotide sequences were detd. on multiple clones of the PCR products. The normal Japanese sequence is identical to - and the chimpanzee sequence differs by only three nucleotides from - a previously published normal Caucasian sequence. In contrast, the two human mutant sequences each differ from the normal

apo C-II gene sequence by several nucleotides, including deletions. The data suggest that both mutant alleles arose >500,000 yr ago. It is shown that a defective allele can persist in a population for only a short time if a bottleneck occurs. Therefore, the antiquity of the two alleles suggests no severe ***bottleneck*** during human ***evolution*** . Moreover, the fact that one allele is from Japan and the other is from a Venezuelan Caucasian family is more consistent with the multiregional evolution model of modern human origins than with the complete replacement or out of Africa model.

L3 ANSWER 42 OF 42 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1986:1554 CAPLUS
DN 104:1554
TI Syrian hamster DNA shows limited polymorphism at class I-like loci
AU McGuire, Kathleen L.; Duncan, William R.; Tucker, Philip W.
CS Southwest. Med. Sch., Univ. Texas, Dallas, TX, 75235, USA
SO Immunogenetics (1985), 22(3), 257-68 CODEN: IMNGBK; ISSN: 0093-7711
DT Journal
LA English
AB The class I gene products of the Syrian hamster major histocompatibility complex are unique in that they lack functionally detectable polymorphism. Mouse cDNA and hamster genomic probes were used to analyze the hamster class I gene family using genomic Southern hybridization. These studies revealed that the hamster possesses a complex class I multigene family and that it shares extensive sequence homol. with the corresponding mouse sequences. Unlike the mouse, however, the Syrian hamster demonstrates only limited restriction endonuclease polymorphism in these genes. Apparently, the lack of detectable polymorphism in this species is directly related to limited DNA polymorphism. The data support the hypothesis that this species has undergone an ***evolutionary*** ***bottleneck*** ; i.e., that all surviving members of the species arose from a limited no. of progenitors.

=> e messier/au
E1 43 MESSIEN P/AU
E2 11 MESSIEN PIERRE/AU
E3 0 --> MESSIER/AU
E4 1 MESSIER A/AU
E5 6 MESSIER A A/AU
E6 1 MESSIER ALAIN/AU
E7 1 MESSIER ALBERT P/AU
E8 2 MESSIER AMBER M/AU
E9 2 MESSIER ANGELA/AU
E10 1 MESSIER ANN MARGARET/AU
E11 1 MESSIER ANTOINETTE/AU
E12 1 MESSIER ARTHUR/AU

=> e messier w/au
E1 13 MESSIER TERRI L/AU
E2 1 MESSIER THEODORE A/AU
E3 0 --> MESSIER W/AU
E4 14 MESSIER WALTER/AU
E5 1 MESSIER YVONNE L/AU
E6 1 MESSIERS CYNTHIA/AU
E7 5 MESSIET J/AU
E8 5 MESSIET JEAN/AU
E9 1 MESSIEZ MUNOZ ANGELA/AU
E10 1 MESSIG M/AU
E11 1 MESSIG MICHAEL/AU
E12 1 MESSIG MICHAEL A/AU

=> s e4
L4 14 "MESSIER WALTER"/AU

=> d l4 1-14 bib ab

L4 ANSWER 1 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2004:311054 CAPLUS
TI Detection of evolutionary bottlenecking by DNA sequencing as a method to discover genes of value
IN ***Messier, Walter***
PA Evolutionary Genomics, LLC, USA
SO PCT Int. Appl., 46 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2004031397 A2 20040415 WO 2003-US25027 20030808 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI US 2002-402340P P 20020808
AB This invention relates to using molecular and evolutionary techniques to identify polynucleotide and polypeptide sequences corresponding to commercially or aesthetically relevant traits in domesticated plants and animals, specifically, a method to detect evolutionary bottleneck sequences.

L4 ANSWER 2 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2004:60212 CAPLUS
DN 140:123638
TI Methods for identification, cloning, transformation and mapping of genes and regulatory sequences involved in plant yield, based on evolutionary sequence changes during domestication
IN ***Messier, Walter***
PA Evolutionary Genomics Llc, USA
SO U.S. Pat. Appl. Publ., 215 pp., Cont.-in-part of U.S. Ser. No. 79,042. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 8 PATENT NO. KIND DATE APPLICATION NO. DATE
PI US 2004016026 A1 20040122 US 2003-345820 20030116 US 6228586 B1 20010508 US 1999-240915 19990129 US 6274319 B1 20010814 US 1999-368810 19990805 US 2004014035 A1 20040122 US 2001-875666 20010606 US 2003148292 A1 20030807 US 2002-79042 20020219
PRAI US 1999-240915 A2 19990129 US 1999-368810 A1 19990805 US 2001-875666 A2 20010606 US 2002-349088P P 20020116 US 2002-349661P P 20020117 US 2002-79042 A2 20020219 US 2002-368541P P 20020329 US 1998-73263P P 19980130 US 1998-98987P P 19980902 US 2001-315595P P 20010829

AB The present invention provides methods for identifying polynucleotide and polypeptide sequences which may be assocd. with com. or aesthetically relevant traits in domesticated plants or animals. The methods employ comparison of homologous genes from the domesticated organism and its ancestor to identify evolutionarily significant changes and evolutionarily neutral changes. Sequences thus identified may be useful in enhancing com. or aesthetically desirable traits in domesticated organisms or their wild ancestors. The examples disclose the discovery of genes EG307 and EG1117 through comparison of modern and ancestral rice (Oryza sativa and O. rufipogon) sequences, and their identification in maize and teosinte. These genes show evidence of pos. selection imposed during domestication by humans.

L4 ANSWER 3 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:609950 CAPLUS
DN 139:144936
TI Methods to identify evolutionarily significant changes in polynucleotide and polypeptide sequences in domesticated plants and animals
IN ***Messier, Walter***
PA Evolutionary Genomics, Llc, USA
SO U.S. Pat. Appl. Publ., 154 pp., Cont.-in-part of U.S. Ser. No. 875,666. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 8 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI US 2003148292 A1 20030807 US 2002-79042 20020219 US 6228586 B1 20010508 US 1999-240915 19990129 US 6274319 B1 20010814 US 1999-368810 19990805 US 2004014035 A1 20040122 US 2001-875666 20010606 WO 2003062382 A2 20030731 WO 2003-US1460 20030116 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG US 2004016026 A1 20040122 US 2003-345820 20030116
PRAI US 1999-240915 A2 19990129 US 1999-368810 A1 19990805 US 2001-875666 A2 20010606 US 2001-315595P P 20010829 US 2002-349088P P 20020116 US 1998-73263P P 19980130 US 1998-98987P P 19980902 US 2002-349661P P 20020117 US 2002-79042 A 20020219 US 2002-368541P P 20020329
AB Sequence comparison methods are used to identify nucleic acid and protein sequences which may be assocd. with com. or aesthetically relevant traits in domesticated plants or animals. The methods employ comparison of homologous genes from the domesticated organism and its ancestor to identify evolutionarily significant changes. Sequences thus identified may be useful in enhancing com. or aesthetically desirable traits in domesticated organisms. CDNA libraries from domesticated plants or animals and their wild counterparts can be screened to clone genes of interest and sequences can be compared to detect synonymous and non-synonymous changes. Use of the method to identify changes assocd. with the domestication of teosinte into maize and the domestication of Oryza rufipogon to O. sativa is demonstrated.

L4 ANSWER 4 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:591297 CAPLUS
DN 139:144923
TI Methods to identify evolutionarily significant changes in polynucleotide and polypeptide sequences in domesticated plants and their use in breeding programs
IN ***Messier, Walter***
PA Evolutionary Genomics Llc, USA
SO PCT Int. Appl., 348 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 8 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2003062382 A2 20030731 WO 2003-US1460 20030116 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG US 2003148292 A1 20030807 US 2002-79042 20020219
PRAI US 2002-349088P P 20020116 US 2002-349661P P 20020117 US 2002-79042 A 20020219 US 2002-368541P P 20020329 US 1999-240915 A2 19990129 US 1999-368810 A1 19990805 US 2001-875666 A2 20010606 US 2001-315595P P 20010829
AB Sequence comparison methods are used to identify nucleic acid and protein sequences which may be assocd. with com. or aesthetically relevant traits in domesticated plants or animals. The methods employ comparison of homologous genes from the domesticated organism and its ancestor to identify evolutionarily significant changes. Sequences thus identified may be useful in enhancing com. or aesthetically desirable traits in domesticated organisms. CDNA libraries from domesticated plants or animals and their wild counterparts can be screened to clone genes of interest and sequences can be compared to detect synonymous and non-synonymous changes. Use of the method to identify changes assocd. with the domestication of teosinte into maize and the domestication of Oryza rufipogon to O. sativa is demonstrated.

L4 ANSWER 5 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:630850 CAPLUS
DN 135:206414
TI Statistical analysis to identify nucleic acid and protein sequences that may be associated with physiological and medical conditions
IN ***Messier, Walter*** ; Sikela, James M.
PA Evolutionary Genomics, L.L.C., USA
SO U.S., 65 pp., Cont.-in-part of U.S. Ser. No. 240,915. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 8 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI US 6280953 B1 20010828 US 2000-591435 20000609 US 6228586 B1 20010508 US 1999-240915 19990129 WO 2001011088 A2 20010215 WO 2000-

US40517 20000801 WO 2001011088 A3 20011213 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BF, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG EP 1250449 A2 20021023 EP 2000-960208 20000801 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL JP 2004500036 T2 20040108 JP 2001-515335 20000801 WO 2001096603 A2 20011220 WO 2001-US18310 20010606 WO 2001096603 A3 20020523 W: AU, CA, JP, US RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR EP 1297180 A2 20030402 EP 2001-942000 20010606 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR JP 2004503251 T2 20040205 JP 2002-510716 20010606
PRAI US 1998-73263P P 19980130 US 1998-98987P P 19980902 US 1999-240915 A2 19990129 US 1999-368810 A 19990805 WO 1999-US20209 W 19990901 US 2000-591435 A 20000609 WO 2000-US40517 W 20000801 WO 2001-US18310 W 20010606
AB The present invention provides methods for identifying polynucleotide and polypeptide sequences in human and/or non-human primates which may be assocd. with a physiol. condition, such as disease (including susceptibility (human) or resistance (chimpanzee) to development of AIDS) or enhanced breast development. The methods employ comparison of human and non-human primate sequences using statistical methods. Sequences thus identified may be useful as host therapeutic targets and/or in screening assays. The methods employ comparison of human and non-human primate sequences using statistical methods, specifically KA/KS (measurement of synonymous and non-synonymous substitution rates) anal. Sequences thus identified may be useful as host therapeutic targets and/or in screening assays. Comparison of intercellular adhesion mols. 1-3 of human and other primates showed that changes in the proteins were the result of pos. selection and may play a role in chimpanzee resistance to AIDS.
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 6 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:592203 CAPLUS
DN 135:163440
TI Methods to identify evolutionarily significant changes in polynucleotide and polypeptide sequences in domesticated organisms and their uses
IN ***Messier, Walter*** ; Sikela, James M.
PA USA
SO U.S., 14 pp., Cont.-in-part of U.S. 6,228,586. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 8 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI US 6274319 B1 20010814 US 1999-368810 19990805 US 6228586 B1 20010508 US 1999-240915 19990129 WO 2001011088 A2 20010215 WO 2000-US40517 20000801 WO 2001011088 A3 20011213 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BF, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG EP 1250449 A2 20021023 EP 2000-960208 20000801 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL JP 2004500036 T2 20040108 JP 2001-515335 20000801 US 2004014035 A1 20040122 US 2001-875666 20010606 US 2003148292 A1 20030807 US 2002-79042 20020219 US 2004016026 A1 20040122 US 2003-345820 20030116
PRAI US 1999-240915 A2 19990129 US 1998-73263P P 19980130 US 1998-98987P P 19980902 US 1999-368810 A 19990805 WO 1999-US20209 W 19990901 US 2000-591435 A 20000609 WO 2000-US40517 W 20000801 US 2001-875666 A2 20010606 US 2001-315595P P 20010829 US 2002-349088P P 20020116 US 2002-349661P P 20020117 US 2002-79042 A2 20020219 US 2002-368541P P 20020329
AB The present invention provides methods for identifying polynucleotide and polypeptide sequences which may be assocd. with com. or aesthetically relevant traits in domesticated organisms. The methods employ comparison of homologous genes from the domesticated organism and its ancestor to identify evolutionarily significant changes. The nucleotide sequences are analyzed by calcg. the no. of non-synonymous changes per site divided by the no. of synonymous changes per site, which may be called KA/KS values. A high KA/KS ratio is assocd. with adaptive evolution, also referred to as pos. selection. Tests for statistical significance can be applied to this mol. evolution anal. Sequences thus identified may be useful in enhancing com. or aesthetically desirable traits in domesticated plants or animals. The methods of this invention were applied to sequences from Genbank for four genes of domesticated corn and teosinte. KA/KS ratios ranging from 0.011 for gene A1* to 0.44-0.89 for gene A1 were obtained, but did not indicate pos. selection.
RE.CNT 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 7 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:115333 CAPLUS
DN 134:173864
TI Identification of evolutionarily significant changes in DNA or protein sequences in domesticated plants and animals by sequence comparison
IN ***Messier, Walter*** ; Sikela, James M.
PA Genoplex, Inc., USA
SO PCT Int. Appl., 46 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 8 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2001011088 A2 20010215 WO 2000-US40517 20000801 WO 2001011088 A3 20011213 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM,

KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BF, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG US 6274319 B1 20010814 US 1999-368810 19990805 WO 2000012764 A1 20000309 WO 1999-US20209 19990901 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG US 6280953 B1 20010828 US 2000-591435 20000609 EP 1250449 A2 20021023 EP 2000-960208 20000801 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL JP 2004500036 T2 20040108 JP 2001-515335 20000801
PRAI US 1999-368810 A 19990805 WO 1999-US20209 W 19990901 US 2000-591435 A 20000609 US 1998-73263P P 19980130 US 1998-98987P P 19980902 US 1999-240915 A2 19990129 WO 1999-US1964 W 19990129 WO 2000-US40517 W 20000801
AB The present invention provides methods for identifying polynucleotide and polypeptide sequences which may be assocd. with com. or aesthetically relevant traits in domesticated plants or animals. The methods employ comparison of homologous genes from the domesticated organism and its ancestor to identify evolutionarily significant changes. Sequences thus identified may be useful in enhancing com. or aesthetically desirable traits in domesticated organisms. CDNA libraries from domesticated plants or animals and their wild counterparts can be screened to clone genes of interest and sequences can be compared to detect synonymous and non-synonymous changes.

L4 ANSWER 8 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:161498 CAPLUS
DN 132:217957
TI Statistical analysis to identify nucleic acid and protein sequences that may be associated with physiological and medical conditions
IN Sikela, James M.; ***Messier, Walter***
PA Genoplex, Inc., USA
SO PCT Int. Appl., 113 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 8 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2000012764 A1 20000309 WO 1999-US20209 19990901 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG WO 9939006 A2 19990805 WO 1999-US1964 19990129 WO 9939006 A3 19991104 W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG AU 9958058 A1 20000321 AU 1999-58058 19990901 WO 2001011088 A2 20010215 WO 2000-US40517 20000801 WO 2001011088 A3 20011213 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BF, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG EP 1250449 A2 20021023 EP 2000-960208 20000801 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL JP 2004500036 T2 20040108 JP 2001-515335 20000801
PRAI US 1998-98987P P 19980902 WO 1999-US1964 W 19990129 US 1998-73263P P 19980130 US 1999-368810 A 19990805 WO 1999-US20209 W 19990901 US 2000-591435 A 20000609 WO 2000-US40517 W 20000801
AB The present invention provides methods for identifying polynucleotide and polypeptide sequences in human and/or non-human primates which may be assocd. with a physiol. condition, such as disease (including susceptibility (human) or resistance (chimpanzee) to development of AIDS). The methods employ comparison of human and non-human primate sequences using statistical methods, specifically KA/KS anal. Sequences thus identified may be useful as host therapeutic targets and/or in screening assays. Comparison of intercellular adhesion mols. 1-3 of human and other primates showed that changes in the proteins were the result of pos. selection and may play a role in chimpanzee resistance to AIDS.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 9 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:495420 CAPLUS
DN 131:112414
TI Methods to identify polynucleotide and polypeptide sequences which may be associated with physiological and medical conditions
IN Sikela, James M.; ***Messier, Walter***
PA Genoplex, Inc., USA
SO PCT Int. Appl., 102 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 8 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 9939006 A2 19990805 WO 1999-US1964 19990129 WO 9939006 A3 19991104 W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG CA 2318772 AA 19990805 CA 1999-2318772 19990129 AU 9924841 A1 19990816 AU

1999-24841 19990129 AU 769931 B2 20040212 EP 1051519 A2 20001115 EP 1999-904442 19990129 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI JP 2002501761 T2 20020122 JP 2000-529463 19990129 WO 2000012764 A1 20000309 WO 1999-US20209 19990901 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG AU 9958058 A1 20000321 AU 1999-58058 19990901
PRAI US 1998-73263P P 19980130 US 1998-98987P P 19980902 WO 1999-US1964 W 19990129 WO 1999-US20209 W 19990901
AB The present invention provides methods for identifying polynucleotide and polypeptide sequences in human and/or non-human primates which may be assocd. with a physiol. condition, such as disease (including susceptibility (human) or resistance (chimpanzee) to development of AIDS). The methods employ comparison of human and non-human primate sequences using statistical methods. Sequences thus identified may be useful as host therapeutic targets and/or in screening assays.

L4 ANSWER 10 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:514326 CAPLUS
DN 129:313900
TI Molecular darwinism: the detection of positive selection on protein-coding genes
AU ***Messier, Walter***
CS State Univ. of New York, Albany, NY, USA
SO (1998) 252 pp. Avail.: UMI, Order No. DA9825796 From: Diss. Abstr. Int., B 1998, 59(3), 985
DT Dissertation
LA English
AB Unavailable

L4 ANSWER 11 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:46008 CAPLUS
DN 126:197891
TI Episodic adaptive evolution of primate lysozymes
AU ***Messier, Walter*** ; Stewart, Caro-Beth
CS Dep. Biol. Sci., Univ. Albany, New York, NY, 12222, USA
SO Nature (London) (1997), 385(6612), 151-154 CODEN: NATUAS; ISSN: 0028-0836
PB Macmillan Magazines
DT Journal
LA English
AB Although the Darwinian concept of adaptation was established nearly a century ago, it has been difficult to demonstrate rigorously that the amino-acid differences between homologous proteins from different species have adaptive significance. There are currently two major types of sequences tests for pos. Darwinian selection on proteins from different species: sequence convergence, and neutral rate violation. Lysozymes from the stomach of cows and langur monkeys, two mammalian species displaying fermn. in the foregut, are an example of amino-acid sequence convergence among homologous proteins. Here the authors combine tests of neutral rate violation with reconstruction of ancestral sequences to document an episode of pos. selection on the lineage leading to the common ancestor of the foregut-fermenting colobine monkeys. This anal. also detected a previously unsuspected adaptive episode on the lineage leading to the common ancestor of the modern hominoid lysozymes. Both adaptive episodes were followed by episodes of neg. selective. Thus this approach can detected adaptive and purifying episodes, and localize them to specific lineages during protein evolution.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 12 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:716559 CAPLUS
TI "Quetzal" coatings
AU Li, Shou-Hsien; ***Messier, Walter***
CS Dep. Biol. Sciences, State Univ. New York, Albany, NY, 12222, USA
SO Science (Washington, D. C.) (1996), 274(5291), 1289
CODEN: SCIEAS; ISSN: 0036-8075
PB American Association for the Advancement of Science
DT Journal; Letter
LA English
AB Unavailable

L4 ANSWER 13 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:341114 CAPLUS
DN 125:27375
TI The birth of microsatellites
AU ***Messier, Walter*** ; Li, Shou-Hsien; Stewart, Caro-Beth
CS Dep. Biological Sciences, Univ. Albany, State Univ. New York, Albany, NY, 12222, USA
SO Nature (London) (1996), 381(6582), 483 CODEN: NATUAS; ISSN: 0028-0836
PB Macmillan Magazines
DT Journal
LA English
AB The independent birth of 2 sep. microsatellites was found in a short region of the .eta.-globin pseudogene in primates. The sequence GT-ATGT-GTGT became GT-GT-GT-GT-GT-GT within New World monkeys (the owl monkey) and the same sequence became GT-ATGT-ATGT within the hominoids, which expanded to GT-(ATGT)4 in the African apes and to GT-(ATGT)5 in humans.

L4 ANSWER 14 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:173293 CAPLUS
DN 122:77058
TI Dissolving the barriers
AU ***Messier, Walter*** ; Stewart, Caro-Beth
CS Dep. Biol. Sci., SUNY, Albany, NY, 12222, USA
SO Current Biology (1994), 4(10), 911-13 CODEN: CUBLE2; ISSN: 0960-9822
PB Current Biology
DT Journal; General Review
LA English
AB A review, with 11 refs. The crystal structure of lysin, a protein involved in abalone fertilization, together with evolutionary sequence anal., provides clues to lysin's non-enzymic mode of action and possible role in speciation.

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(FILE 'HOME' ENTERED AT 14:11:25 ON 27 APR 2004)
FILE 'STNGUIDE' ENTERED AT 14:11:30 ON 27 APR 2004
FILE 'HOME' ENTERED AT 14:11:35 ON 27 APR 2004
FILE 'CAPLUS' ENTERED AT 14:11:44 ON 27 APR 2004
L1 60 S (EVOLUT? (3A) BOTTLE?)/BI,AB

L2 58 S L1 NOT 2004/PY
L3 42 S (EVOLUT? (3A) BOTTLEN?)/BI,AB E MESSIER/AU E MESSIER W/AU
L4 14 S E4

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